

SEQUENCE LISTING

<110> CropDesign N.V.
 <120> Plants having modified growth characteristics and method for making the same
 <130> 1187-30
 <150> PCT/EP2004/053594
 <151> 2004-12-17
 <150> EP 03104764.0
 <151> 2003-12-17
 <150> US 60/531,866
 <151> 2003-12-22
 <160> 7
 <170> PatentIn version 3.3
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 <211> 1380
 <212> DNA
 <213> Nicotiana tabacum
 <400> 1
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 catgtcaata atttttcatc acatcccccta aatacaaggc aagatcaaca accttcatat 180
 acaaaaactt cgctcaaaaa accaagtaat tctgatcaaa gaattgagaa tatatgtgaa 240
 attcagttca acaaaagtga atcaaaggat gggtttgatc catttggtga attagtcact 300
 tctgggaaga gaaacccaaa agggatttca cttactaatg tggttgaaatg ccctgtctgt 360
 ggtagtggtt ttgtttctga agaagagggtg tcaactcata ttgatagctg tttaagttct 420
 gaagtgtctt ctaatttggg agttgaaagt aaagttgaag ttaaaagtga attggaaaca 480
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gcaagaaaaga agtacacaaa atccattatc cgtgtacagt ttccagatgg agcattgctt 1080
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<210> 2
<211> 459
<212> PRT
<213> Nicotiana tabacum

<400> 2

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Ser Ser Ser Ser Gly Lys Phe Lys Gly Gln Gly Arg Val Leu Gly Gly
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Ser Ser Ser Ser Gly Pro Ser Asn His Val Asn Asn Phe Ser Ser His
35 40 45

Pro Leu Asn Thr Arg Gln Asp Gln Gln Pro Ser Tyr Thr Lys Thr Ser
50 55 60

Pro Gln Lys Pro Ser Asn Ser Asp Gln Arg Ile Glu Asn Ile Cys Glu
65 70 75 80

Ile Gln Phe Asn Lys Ser Glu Ser Lys Asp Gly Phe Asp Pro Phe Gly
85 90 95

Glu Leu Val Thr Ser Gly Lys Arg Asn Pro Lys Gly Tyr Ser Leu Thr
100 105 110

Asn Val Phe Glu Cys Pro Val Cys Gly Ser Gly Phe Val Ser Glu Glu
115 120 125

Glu Val Ser Thr His Ile Asp Ser Cys Leu Ser Ser Glu Val Ser Ser
130 135 140

Asn Leu Gly Val Glu Ser Lys Val Glu Val Lys Ser Glu Leu Glu Thr
145 150 155 160

Cys Val Ser Ala Tyr Val Ser Gly Lys Pro Ser Glu Gly Ser Val Glu
165 170 175

Val Val Ile Lys Leu Leu Lys Asn Ile Val Lys Glu Pro Glu Asn Ala
180 185 190

Lys Phe Arg Lys Ile Arg Met Gly Asn Pro Lys Ile Lys Gly Ala Ile
195 200 205

Gly Asp Val Val Gly Gly Val Glu Leu Leu Glu Phe Val Gly Phe Glu
210 215 220

Leu Lys Glu Glu Gly Gly Glu Ile Trp Ala Val Met Asp Val Pro Ser
225 230 235 240

Glu Glu Gln Leu Val Met Leu Lys Asn Val Val Ser Leu Leu Glu Pro
245 250 255

Lys Lys Val Glu Glu Leu Ala Ser Leu Ser Gln Val Lys Ala Ser Glu
260 265 270

Pro Val Glu Pro Lys Lys Ile Asp Arg Gln Ile Arg Val Phe Phe Ser
275 280 285

Val Pro Glu Ser Val Ala Ala Lys Ile Glu Leu Pro Asp Ser Phe Phe
290 295 300

Asn Leu Ser Arg Glu Glu Leu Arg Arg Glu Ala Glu Met Arg Lys Lys
305 310 315 320

Lys Leu Glu Asp Ser Lys Leu Leu Ile Pro Lys Ser Tyr Arg Glu Lys
325 330 335

Gln Ala Lys Ala Ala Arg Lys Lys Tyr Thr Lys Ser Ile Ile Arg Val
340 345 350

Gln Phe Pro Asp Gly Ala Leu Leu Gln Gly Val Phe Leu Pro Ser Glu

355

360

365

Pro Thr Ser Ala Leu Tyr Glu Phe Val Ser Ala Ala Leu Lys Glu Pro
 370 375 380

Ser Leu Glu Phe Glu Leu Leu His Pro Val Leu Val Lys Lys Arg Val
 385 390 395 400

Ile Pro His Phe Pro Ala Ala Gly Glu Arg Ala Val Thr Val Glu Glu
 405 410 415

Glu Asp Leu Val Pro Ala Ala Leu Leu Lys Phe Lys Pro Ile Glu Thr
 420 425 430

Asp Ser Val Val Phe Thr Gly Leu Cys Asn Glu Leu Leu Glu Ile Ser
 435 440 445

Glu Pro Leu Glu Thr Gly Ser Val Ala Ser Ser
 450 455

<210> 3
 <211> 1311
 <212> DNA
 <213> Saccharum officinarum

<220>
 <221> misc_feature
 <222> (277)..(279)
 <223> n can be any nucleotide

<400> 3
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 caccccgtg cccgctcctc aaaccctagc ccaaacctca ggcccgtcc taagcggacc 180
 tcgccaccta ccccgccac tttaaccacc gatttgacct ccttcacgcc cctcgtctgc 240
 tactcctccc gcgcgccga cgogaacggc accgcgnnng ccgtcgccac cgtcgcgtgc 300
 cccagctgcg gagacgcgtt tccgtccgag ctcgccgtct ccgagcatct cgacggctgc 360
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 ggcaacgata agttcaggcg ggtgagattg ggtaaccgc ggatcaagga ggccctggca 540

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cggcagattc gggatattgt ctctgttcct gggagttcta tggcacaaaa tgatgtacca 840
gattcttttt acaagcttag tggtagaggag ataaggaatg aagcaaagat gaggagggaa 900
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ccatctgcgc tcctcaagtt cattcccaag gagactgatt ccatggtttt caccggtttg 1260
cttgatgagc ttctcatggc cagtgagccg cttcctgctg catcacaatg a 1311

<210> 4
<211> 436
<212> PRT
<213> Saccharum officinarum

<220>
<221> MISC_FEATURE
<222> (93)..(93)
<223> Xaa can be any amino acid

<400> 4

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Ser Gly Pro Ser Pro Ser Ser Ser His Pro Ala Ala Arg Ser Ser Asn
35 40 45

Pro Ser Pro Asn Leu Arg Pro Ala Pro Lys Arg Thr Ser Pro Pro Thr
50 55 60

Pro Pro Thr Leu Thr Thr Asp Leu Thr Ser Phe Thr Pro Leu Val Cys

65	70	75	80
Tyr Ser Ser Arg Arg Pro Asp Ala Asn Gly Thr Ala Xaa Ala Val Ala	85	90	95
Thr Val Ala Cys Pro Ser Cys Gly Asp Ala Phe Pro Ser Glu Leu Ala	100	105	110
Val Ser Glu His Leu Asp Gly Cys Leu Ala Ser Ala Gly Gly Ala Arg	115	120	125
Ala Arg Ala Ala Ala Tyr Leu Ala Ala Asp Pro Pro Pro Pro Ala Ala	130	135	140
Ser Val Glu Val Val Lys Arg Leu Leu Gly Asn Leu Leu Arg Glu Pro	145	150	155
Gly Asn Asp Lys Phe Arg Arg Val Arg Leu Gly Asn Pro Arg Ile Lys	165	170	175
Glu Ala Leu Ala Asp Arg Asp Gly Gly Val Glu Leu Leu Glu Ala Val	180	185	190
Gly Phe Thr Val Gly Asp Glu Gly Gly Glu Pro Phe Ala Val Met Asp	195	200	205
Glu Val Pro Ser Asp Pro Arg Leu Asn Gly Ile Arg Arg Ala Val Leu	210	215	220
Leu Leu Glu Gly Ala His Pro Ser Ala Pro Pro Val Lys Ala Glu Ala	225	230	235
Glu Ala Lys Glu Ser Cys Ser Asn Val Ser Asp Val Gln Glu Gly Ala	245	250	255
Lys Thr Ile Asp Arg Gln Ile Arg Val Phe Val Ser Val Pro Gly Ser	260	265	270
Ser Met Ala Gln Asn Asp Val Pro Asp Ser Phe Tyr Lys Leu Ser Gly	275	280	285
Glu Glu Ile Arg Asn Glu Ala Lys Met Arg Arg Glu Arg Leu Glu Gln	290	295	300

Ser Arg Leu Leu Ile Pro Lys Ser Tyr Lys Glu Lys Gln Ala Leu Ala
 305 310 315 320

Ala Arg Gln Lys Tyr Lys Gln Ala Val Ile Arg Val Gln Phe Pro Asp
 325 330 335

Arg Met Ile Leu Gln Gly Ile Phe Leu Pro Gly Glu Ala Thr Ser Ser
 340 345 350

Leu Tyr Glu Phe Val Thr Ser Ala Leu Lys Gln Ser Gly Leu Glu Phe
 355 360 365

Glu Leu Ile Ser Pro Ala Ile Pro Lys Pro Arg Val Val Pro His Phe
 370 375 380

Pro Asn Pro Gly Glu Arg Ala Arg Thr Leu Gln Glu Glu Glu Leu Val
 385 390 395 400

Pro Ser Ala Leu Leu Lys Phe Ile Pro Lys Glu Thr Asp Ser Met Val
 405 410 415

Phe Thr Gly Leu Leu Asp Glu Leu Leu Met Ala Ser Glu Pro Leu Pro
 420 425 430

Ala Ala Ser Gln
 435

<210> 5
 <211> 3048
 <212> DNA
 <213> Artificial sequence

<220>
 <223> expression cassette comprising GRUBX (1011-2390) operably linked
 to the prolamine promoter (1-654) and the T-Zein + T-Rubisco
 deltaG terminator (2615-2808 and 2852-3048)

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 ttattgtaaa gttctacaaa gctaatttaa aagttattgc attaacttat ttcattattac 180
 aaacaagagt gtcaatggaa caatgaaaac catatgacat actataattt tgttttttatt 240

attgaaatta tataattcaa agagaataaa tccacatagc cgtaaagttc tacatgtggt	300
gcattaccaa aatatatata gcttacaaaa catgacaagc ttagtttgaa aaattgcaat	360
ccttatcaca ttgacacata aagtgagtga tgagtcataa tattattttc tttgctaccc	420
atcatgtata tatgatagcc acaaagttac tttgatgatg atatcaaaga acatttttag	480
gtgcacctaa cagaatatcc aaataatatg actcacttag atcataatag agcatcaagt	540
aaaactaaca ctctaaagca accgatggga aagcatctat aaatagacaa gcacaatgaa	600
aatcctcatc atccttcacc acaattcaaa tattatagtt gaagcatagt agtaatttaa	660
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gtttgaattg attgattgac agatttttgt gagaggggtg tattgaaaaa atgggtgaca	1020
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aaggccaagg tagggttttg ggtggttcat cttcttcagg acctcaaatt catgtcaata	1140
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attccaaatt attgattcct aaatcttatac gggaaaagca ggcaaaagct gcaagaaaga	2040
agtacacaaa atccattatac cgtgtacagt ttccagatgg agcattgctt caaggtgtct	2100
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 <212> DNA
 <213> *Oryza sativa*

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tccgcgccct ccaacctac ccctagtcgc cccgctgccc cccggcgaga ggccgcccgc	180
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agctgcgccg agccgttccc ctccgagctg gcggtgtcgg accacctga cggctgcctc	360
gcggcgccgg ggggagccc ccccgccgc gccgcctacc tggccggcga cccccccgcg	420

Arg Arg Thr Asp Pro Pro Ala Gly Ala Gly Ala Gly Glu Asp Asp Ala
85 90 95

Val Ala Cys Pro Ser Cys Ala Glu Pro Phe Pro Ser Glu Leu Ala Val
100 105 110

Ser Asp His Leu Asp Gly Cys Leu Ala Ala Ala Gly Gly Ala Arg Pro
115 120 125

Arg Ala Ala Ala Tyr Leu Ala Gly Asp Pro Pro Ala Ser Ala Val Glu
130 135 140

Val Val Lys Arg Leu Leu Gly Asn Leu Leu Ser Asp Pro Arg Asn Asp
145 150 155 160

Lys Tyr Arg Lys Val Arg Leu Gly Asn Pro Arg Ile Lys Glu Ala Leu
165 170 175

Ala Asp Arg Glu Gly Gly Val Asp Leu Leu Glu Ala Val Gly Phe Arg
180 185 190

Val Ala Asp Glu Gly Gly Glu Leu Phe Ala Leu Met Asp Glu Val Pro
195 200 205

Gly Asp Ala Arg Leu Gly Gly Ile Arg Gln Ala Val Leu Leu Leu Glu
210 215 220

Arg Ala Arg Pro Ser Thr Pro Pro Gln Thr Gln Ala Asp Ala Lys Glu
225 230 235 240

Thr Cys Pro Asn Gly Val Ser Glu Glu Gln Gly Ile Lys Lys Pro Val
245 250 255

Asp Arg Gln Ile Arg Val Phe Phe Ser Val Ala Ala Ser Ser Val Ala
260 265 270

Glu Asn Asp Leu Pro Asp Ser Phe Tyr Ser Leu Ser Asn Glu Glu Ile
275 280 285

Arg Asn Glu Ala Lys Met Arg Arg Glu Arg Leu Glu Gln Ser Arg Leu
290 295 300

Leu Ile Pro Lys Ser Tyr Lys Glu Lys Gln Ala Leu Ala Ala Arg Gln
305 310 315 320

Lys Tyr Lys Gln Ala Leu Ile Arg Ile Gln Phe Pro Asp Gly Val Ile
325 330 335

Leu Gln Gly Val Phe Leu Pro Ala Glu Pro Ile Ser Ser Leu Tyr Glu
340 345 350

Phe Val Ala Ser Ser Leu Lys Gln Pro Ser Leu Glu Phe Asp Leu Ile
355 360 365

Cys Pro Ala Gly Pro Arg Thr Arg Val Ile Pro Pro Phe Pro Lys Pro
370 375 380

Gly Glu Gln Ala Arg Thr Leu Arg Asp Glu Asp Leu Val Pro Ser Ala
385 390 395 400

Arg Leu Thr Phe Lys Pro Lys Glu Thr Asp Ser Val Val Phe Thr Gly
405 410 415

Leu Leu Asp Glu Leu Leu Glu Thr Ser Glu Pro Phe Thr Ser Ala Ser
420 425 430

Ser